

Amendments to the Claims:

1, 7, 9, 14, 15, 26, 28-30, 36-38, 40-42, 45-47,

The following listing of claims will replace all prior versions, and listings, of claims in

the application:

(1) (Previously Amended) An isolated polynucleotide, comprising a nucleic acidhaving a nucleotide sequence selected from the group consisting of:

(i) sequences SEQ ID NO: 6, SEQ ID NO: 9, and SEQ ID NO: 12;

(ii) sequences complementary to sequences (i); and(iii) sequences having, for every series of 100 contiguous monomers, at least 70%identity with sequences (i) or (ii).

2-6. (Canceled)

(7) (Previously Presented) An isolated retroviral polynucleotide comprising an

env gene, wherein said env gene comprises a nucleic acid having a nucleotide sequence selected from the group consisting of SEQ ID NO: 9, its complementary sequence, and sequences having, for every series of 100 contiguous monomers, at least 70% identity with SEQ ID NO: 9 or said complementary sequence.

8. (Canceled)

(9) (Previously Presented) An isolated retroviral polynucleotide comprising an env gene, wherein said env gene encodes a polypeptide having, for every contiguous series of at least 30 amino acids, at least 70% identity with the peptide sequence SEQ ID NO: 10.

10-13. (Canceled)

(14) (Previously Presented) An isolated fragment comprising a polynucleotide

having a nucleotide sequence selected from the group consisting of:

(i) sequences SEQ ID NO: 6, SEQ ID NO: 9, and SEQ ID NO: 12;(ii) sequences complementary to sequences (i); and(iii) sequences having, for every series of 100 contiguous monomers, at least 70%identity with sequences (i) or (ii).

102 (b)

(15) (Previously Presented) The fragment according to Claim 14, consisting of a polynucleotide having a nucleotide sequence selected from the group consisting of:

(i) sequences SEQ ID NO: 6, SEQ ID NO: 9, and SEQ ID NO: 12;

(ii) sequences complementary to sequences (i); and

(iii) sequences having, for every series of 100 contiguous monomers, at least 70% identity with sequences (i) or (ii).

16-25. (Canceled)

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(26) (Previously Presented) A method for detecting a retrovirus associated with multiple sclerosis and/or rheumatoid arthritis, in a biological sample, characterized in that an RNA and/or a DNA assumed to belong to or obtained from said retrovirus, or their complementary RNA and/or DNA, is brought into contact with a composition comprising a nucleotide fragment according to claim 14.

27. (Canceled)

(28) (Previously Presented) The polynucleotide of claim 1, wherein the nucleic acid has a nucleotide sequence having for every series of at least 100 contiguous monomers, at least 80% identity with the sequences (i) or (ii).

(29) (Previously Presented) The polynucleotide of claim 1, wherein the nucleic acid has a nucleotide sequence having for every series of at least 100 contiguous monomers, at least 90% identity with the sequences (i) or (ii).

(30) (Previously Presented) The polynucleotide of claim 1, wherein the nucleic acid has a nucleotide sequence having for every series of at least 100 contiguous monomers, at least 95% identity with the sequences (i) or (ii).

31-35. (Canceled)

(36) (Previously Presented) The retroviral polynucleotide of claim 7, wherein the nucleic acid has a nucleotide sequence having, for every series of at least 100 contiguous

monomers, at least 80% identity with the nucleotide sequences selected from the group consisting of SEQ ID NO: 9, and its complementary sequences.

(37) (Previously Presented) The retroviral polynucleotide of claim 7, wherein the nucleic acid has a nucleotide sequence having, for every series of at least 100 contiguous monomers, at least 90% identity with the nucleotide sequences selected from the group consisting of SEQ ID NO: 9, and its complementary sequences.

(38) (Previously Presented) The retroviral polynucleotide of claim 7, wherein the nucleic acid has a nucleotide sequence having, for every series of at least 100 contiguous monomers, at least 95% identity with the nucleotide sequences selected from the group consisting of SEQ ID NO: 9, and its complementary sequences.

39. (Canceled)

(40) (Previously Presented) The isolated retroviral polynucleotide of claim 9, wherein the env gene encodes a polypeptide having, for every contiguous series of at least 30 amino acids, at least 80% identity with the peptide sequence SEQ ID NO: 10.

(41) (Previously Presented) The isolated retroviral polynucleotide of claim 9, wherein the env gene encodes a polypeptide having, for every contiguous series of at least 30 amino acids, at least 90% identity with the peptide sequence SEQ ID NO: 10.

(42) (Previously Presented) The isolated retroviral polynucleotide of claim 9, wherein the env gene encodes a polypeptide having, for every contiguous series of at least 30 amino acids, at least 95% identity with the peptide sequence SEQ ID NO: 10.

43-44. (Canceled)

(45) (Previously Presented) The polynucleotide fragment according to claim 14, wherein said fragment has, for every series of 100 contiguous monomers, at least 80% identity with the nucleic acid sequences of (i) or (ii).

(46) (Previously Presented) The polynucleotide fragment according to claim 14, wherein said fragment has, for every series of 100 contiguous monomers, at least 90% identity with the nucleic acid sequences of (i) or (ii).

(47) (Previously Presented) The polynucleotide fragment according to claim 14, wherein said fragment has, for every series of 100 contiguous monomers, at least 95% identity with the nucleic acid sequences of (i) or (ii).

48. (Canceled)

(49) (Previously Presented) The polynucleotide fragment according to claim 15, wherein said fragment has, for every contiguous series of 100 contiguous monomers, at least 80% identity with the nucleic acid sequences of (i) or (ii).

(50) (Previously Presented) The polynucleotide fragment according to claim 15, wherein said fragment has, for every contiguous series of 100 contiguous monomers, at least 90% identity with the nucleic acid sequences of (i) or (ii).

(51) (Previously Presented) The polynucleotide fragment according to claim 15, wherein said fragment has, for every contiguous series of 100 contiguous monomers, at least 95% identity with the nucleic acid sequences of (i) or (ii).

52-59. (Canceled)

102(b) (60) (Previously Presented) The isolated polynucleotide according to claim 1, wherein said polynucleotide is DNA.

(61) (Previously Presented) The isolated polynucleotide according to claim 1, wherein said polynucleotide is RNA.

(62) (Previously Presented) The isolated polynucleotide according to claim 1, wherein said polynucleotide is genomic DNA. → ? IN RESEQUENCING WHAT? A CHROMOSOME? WHICH ANIMAL?

(63) (Previously Presented) A recombinant vector comprising the polynucleotide defined in claim 1.

sequence selected from the group consisting of SEQ ID NO: 6, a complement of SEQ ID NO: 6, SEQ ID NO: 9, a complement of SEQ ID NO: 9, SEQ ID NO: 12, and a complement of SEQ ID NO: 12.

56 (New) The isolated polynucleotide of claim 65, wherein said nucleotide is selected from the group consisting of SEQ ID NO: 6, a complement of SEQ ID NO: 6, SEQ ID NO: 9, and a complement of SEQ ID NO: 9.